

## SEQUENZPROTOKOLL

&lt;110&gt; Degussa AG

5 &lt;120&gt; Neue für das luxS-Gen kodierende Nukleotidsequenzen

&lt;130&gt; 000457 BT

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 4

15 &lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1902

&lt;212&gt; DNA

20 &lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (342)..(1610)

25 &lt;223&gt; luxS-Gen

&lt;400&gt; 1

ggtaggagta aaaaacgcag gagggcgtcg aaaagcgttc gtctgtgccg taacccgtga 60

30 cgcgctggcc gttggtatcg gcgaccaggc cggtgcccag ttagggcat gcggtttgcg 120

cggtgcgttc gaccgcgggc atcgcgtcga tggaaaggcc gtcagtaatt acttccgggg 180

ctgcctcggt ggtggtctct ggggttgctt caggttccgc cgggttacaa gcggtgagca 240

35 tgatggaagc agcgaggata ttaggtaatg tacgacgcat gcagtcaagc cttagatcgtg 300

tgtcgaaac cggacgcaat gagctcgatg ttgaaaccct t gtg aag aag ggg aat 356

Met Lys Lys Gly Asn

1 5

40 caa ccg ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404

Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala  
10 15 20

45 tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452

Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro  
25 30 35

50 atg ttt gcg ctg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500

Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr  
40 45 50

55 ttc tat gga tca acc aaa cgc gta gat ttg agc cac ggc atg cag ctg 548

Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu  
55 60 65

60 ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc 596

Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile  
70 75 80 85

	gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta	644
	Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu	
	90 95 100	
5	cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca	692
	Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr	
	105 110 115	
10	gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt	740
	Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly	
	120 125 130	
15	gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac	788
	Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr	
	135 140 145	
20	gct ttc cgc acg ttg tgg cgg gtg aat aat gaa aag cag gaa ttg att	836
	Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile	
	150 155 160 165	
25	gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat	884
	Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn	
	170 175 180	
30	gct ggt att gct gcg gaa cgt caa cgt att gcg cat gaa att cat gac	932
	Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp	
	185 190 195	
35	acg gtc gcc cag gga ctc tcc att caa atg ctg ctg cat gtc tct	980
	Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser	
	200 205 210	
40	gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg	1028
	Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala	
	215 220 225	
45	atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc	1076
	Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu	
	230 235 240 245	
50	agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct	1124
	Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser	
	250 255 260	
55	aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg	1172
	Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu	
	265 270 275	
50	ggt att aat ttt gtg att tct gtc gac ggt gat gtt cgc caa ctg ccc	1220
	Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro	
	280 285 290	
55	atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga	1268
	Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly	
	295 300 305	

	aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc	1316		
	Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr			
310	315	320		
5	tac gaa gac aca gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt	1364		
	Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly			
	330	335	340	
10	ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc	1412		
	Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile			
	345	350	355	
15	ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt	1460		
	Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val			
	360	365	370	
20	ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg	1508		
	Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu			
	375	380	385	
25	ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat	1556		
	Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp			
	390	395	400	405
30	tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac	1604		
	Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp			
	410	415	420	
35	gat gag taaggctaga ctaaagtacg attcatctgc tcatcgatac tcttgaaggc	1660		
	Asp Glu			
	gcattttcat tcgaaaacgaa gtgcgccatt gggaggacc tagttcaaac aatgattcgc	1720		
	gtgctgcttg ctgatgacca cgaaatcgtg aggctcgac tccgagctgt gctggaaagc	1780		
	gccgaggaca ttgaagtgg gggcgaaagtc tccaccgccc aaggtgcgt gcaggcagcc	1840		
	caagaaggcg gaatcgacgt catttgatg gacctccgat tcggccccgg cgtccaagga	1900		
40	ac	1902		
	<210> 2			
45	<211> 423			
	<212> PRT			
	<213> Corynebacterium glutamicum			
	<400> 2			
50	Met Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile			
	1 5 10 15			
	His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala			
	20 25 30			
55	Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val			
	35 40 45			
	Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser			
	50 55 60			

His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile  
65 70 75 80

5 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu  
85 90 95

Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala  
100 105 110

Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly  
115 120 125

Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr  
15 130 135 140

Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu  
145 150 155 160

20 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala  
165 170 175

Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala  
180 185 190

25 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met  
195 200 205

Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu  
30 210 215 220

Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr  
225 230 235 240

35 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln  
245 250 255

Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val  
260 265 270

40 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp  
275 280 285

Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala  
45 290 295 300

Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys  
305 310 315 320

50 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val  
325 330 335

Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala  
340 345 350

55 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu  
355 360 365

Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala  
370 375 380

5 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala  
385 390 395 400

Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu  
405 410 415

10 Ser Ser Pro Thr Asp Asp Glu  
420

15 <210> 3  
<211> 20  
<212> DNA  
<213> *Corynebacterium glutamicum*

20 <220>  
<223> Primer luxS-int1

<400> 3  
tcgtgaccgt ggctattgat 20

25 <210> 4  
<211> 20  
<212> DNA  
30 <213> *Corynebacterium glutamicum*

<220>  
<223> Primer luxS-int2

35 <400> 4  
cttgagcaat tcgcagaagg 20